





XX 07-AUG-2000 (first entry)  
 DT NCAM Igl binding peptide 120 used as a control peptide.  
 DE NCAM Igl binding peptide 120 used as a control peptide.  
 XX NCAM: neural cell adhesion molecule, Ig1, immunoglobulin domain 1;  
 XX neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 KW treatment; prosthetic nerve guide; treatment; nervous system.  
 XX Synthetic.  
 OS Synthetic.  
 XX WO200018801-A2.  
 PN 06-APR-2000.  
 PD 23-SEP-1999; 99WO-DK00500.  
 XX 29-SEP-1999; 99TK-0001332.  
 PR 29-APR-1999; 99TK-0000592.  
 XX (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F M.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX P-444 LCB, BOCK E, HOLM A, OLSEN M, OSTERGAARD S, JENSEN PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX WPI: 2000-293111/25.  
 XX Compositions that bind neural cell adhesion molecules useful for  
 PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
 PT and Parkinson's diseases -  
 XX Example 5; Fig 7; 119pp; English.  
 XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting of five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The invention relates to a compound containing a peptide  
 CC which binds to the NCAM Igl domain. The compound binds to NCAM-Igl/Ig2  
 CC domain, and is capable of stimulating or promoting neurite outgrowth  
 CC from NCAM presenting cells, and is also capable of promoting the  
 CC proliferation of NCAM presenting cells. The present sequence represents a  
 CC control peptide used in the identification of those binding peptides  
 CC which can be used in the compound. The compound may be used in the  
 CC treatment of normal, degenerated or damaged NCAM presenting cells. The  
 CC compound may in particular be used to treat diseases of the central and  
 CC peripheral nervous systems such as post operative nerve damage, traumatic  
 CC nerve damage, impaired myelination of nerve fibres, conditions resulting  
 CC from a stroke, Parkinson's disease, Alzheimer's disease, dementia,  
 CC sclerosis, nerve degeneration associated with diabetes mellitus,  
 CC disorders affecting the circadian clock or neuro-muscular transmission  
 CC and schizophrenia. Conditions affecting the muscles may also be treated  
 CC with the compound, such as conditions associated with impaired function  
 CC of neuromuscular connectors (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject.  
 CC Sequence 11 AA:

Query Match  
 Best Local Similarity 90.9%; Pred No. 0.057;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 YY 1 ASKKKRNITK 11  
 DB 1 ASKKAKRNITK 11  
 RESULT 4  
 ID AAY88554  
 XX AAY88554 standard; peptide; 11 AA.  
 AC AAY88554;  
 XX 07-AUG-2000 (first entry)  
 DT NCAM Igl binding peptide 117 used as a control peptide.  
 DE NCAM Igl binding peptide 117 used as a control peptide.  
 XX NCAM: neural cell adhesion molecule, Ig1, immunoglobulin domain 1;  
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 KW treatment; prosthetic nerve guide; treatment; nervous system.  
 XX Synthetic.  
 OS Synthetic.  
 XX WO200018801-A2  
 PN 06-APR-2000.  
 PD 23-SEP-1999; 99WO-DK00500.  
 XX 29-SEP-1999; 99TK-0001332.  
 PR 29-APR-1999; 99TK-0000592.  
 XX (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F M.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX Ronn LCB, BOCK E, HOLM A, OLSEN M, OSTERGAARD S, JENSEN PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX WPI: 2000-293111/25.  
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 PT and Parkinson's diseases -  
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 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The invention relates to a compound containing a peptide  
 CC which binds to the NCAM Igl domain. The compound binds to NCAM-Igl/Ig2  
 CC domain, and is capable of stimulating or promoting neurite outgrowth  
 CC from NCAM presenting cells, and is also capable of promoting the  
 CC proliferation of NCAM presenting cells. The present sequence represents a  
 CC control peptide used in the identification of those binding peptides  
 CC which can be used in the compound. The compound may be used in the  
 CC treatment of normal, degenerated or damaged NCAM presenting cells. The  
 CC compound may in particular be used to treat diseases of the central and



PS Example 7; Page 32; 50pp; English.

CC To determine which amino acids within the HTLV-I envelope amino  
 CC acids 88-98 were required for absorption of neutralising anti-peptide  
 CC antibodies to HTLV-I, 11 peptides (221.1-221.11) were synthesised in  
 CC which sequential amino acids were each replaced by the amino acid  
 CC alanine. These 11 mutated peptides, as well as peptide 221.1 bearing the  
 CC native HTLV-I sequence were tested and identified that amino acids 90,  
 CC 92, 93 and 95 were important for HTLV-I neutralisation.  
 CC See also NAF3425 57.

XX Sequence 11 AA;

SO Query Match 61.1%; Score 33; DB 14; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 15;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASKPPEN 8  
 | | | | |  
 DB 1 ATKPPEN 9

RESULT 7  
 AAR95642  
 ID AAR95642 standard; Peptide; 13 AA.  
 XX AAR95642;  
 XX 46-NOV-1990 (first entry)  
 XX Antigen peptide from cartilage-derived morphogenetic protein 1.  
 XX Human; antigen; cartilage-derived morphogenetic protein-1; CDMP-1;  
 XX Polyclonal antibody; rabbit; articular cartilage; chondrogenic;  
 XX vulnereary; implantation; chondromatolacia; osteoarthritis; therapy;  
 XX joint repair.  
 XX Homo sapiens.  
 XX WO9614335-A1.  
 XX 17-MAY-1996.  
 XX 07-NOV-1994; 94WO-US12814.  
 XX 07-NOV-1994; 94WO-US12814.  
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX Chang SC, Luyten FP, Moos M,  
 XX WPI: 1996-251714/25.  
 XX New purified cartilage extracts and proteins - used to stimulate the  
 XX development and repair of cartilage in vivo.  
 XX Example 7; Page 15; 34pp; English.

XX This peptide antigen is derived from the mature C-terminal domain  
 CC of human articular cartilage-derived morphogenetic protein-1 (CDMP-1,  
 CC AAR95642) and has been used to generate polyclonal antibodies in  
 CC rabbits. The peptide does not show sequence identity with any  
 CC other known protein, including bone morphogenetic protein. The  
 CC resulting antibodies have been used to screen tissues from human  
 CC embryos, to study differential CDMP gene expression. At 6 wk,  
 CC CDMP-1 is detected in precartilaginous condensations, and at 7.5-8.5 wk  
 CC CDMP-1 is found in cartilaginous cores of long bones. In areas of  
 CC active cartilage degradation and bone matrix formation, CDMP-1  
 CC expression is also detected in hypertrophic chondrocytes. No  
 CC expression is detected in the axial skeleton, and only low levels  
 CC are present in other tissues. CDMP-1 is present in a purified  
 CC cartilage extract (eluted) which stimulates local cartilage  
 CC formation and repair when combined with a matrix and implanted

CC in a mammal. The protein may be used in therapy of e.g.  
 CC chondromatolacia or osteoarthritis, to heal joint surfaces, or to  
 CC repair cartilage after reconstructive surgery.

XX Sequence 13 AA;

SO Query Match 61.1%; Score 33; DB 17; Length 13;  
 Best Local Similarity 55.6%; Pred. No. 17;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKPKRNKA 11  
 | | | | |  
 DB 3 KRPKNKA 11

RESULT 8  
 AAY88556  
 ID AAY88556 standard; peptide; 11 AA.  
 XX AAY88556;  
 XX 07-AUG-2000 (first entry)  
 XX NCAM Ig1 binding peptide 119 used as a control peptide.  
 XX NCAM  
 XX NCAM: neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
 XX neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 XX impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 XX Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 XX treatment; prosthetic nerve guide; treatment; nervous system.  
 XX Synthetic.  
 XX WU200018601-A2.  
 XX 06-APR-2000.  
 XX 23-SEP-1999; 99WO-DK00500.  
 XX 29-SEP-1999; 99NK-0002232.  
 XX 29-APR-1999; 99NK-0006592.  
 XX (RONN/) RONN L C B.  
 XX (BOCK/) BOCK E.  
 XX (HOLM/) HOLM A.  
 XX (OLSE/) OLSEN M.  
 XX (OSTE/) OSTERGAARD S.  
 XX (JENS/) JENSEN P H.  
 XX (POUL/) POULSEN F M.  
 XX (SCRO/) SCROKA V.  
 XX (RALE/) RALETS I.  
 XX (BERE/) BEREZIN V.  
 XX Romm LOB, Bock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH;  
 XX Poulsen FM, SCROKA V, RALETS I, BEREZIN V;  
 XX WPI: 2000-293111/25.  
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 CC N-terminal. The invention relates to a compound containing a peptide  
 CC which binds to the NCAM Ig domain. The compound binds to NCAM Ig domain  
 CC domains, and is capable of stimulating or promoting neurite outgrowth  
 CC from NCAM presenting cells, and is also capable of promoting the









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OM protein Protein search using SW model

Run on March 20, 2003, 11:49:50, Search time 16 Seconds  
(without alignments)  
66.092 Million cell updates/sec

File: US-09-787-443-1

Sequence: 1 ASKPPKPNHVA 11

Scoring table: PROSUM62  
Gapop 10.0, Gapext 0.5

Searched: 293224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0

Maximum DB seq length: 20

Post processing: Minimum Match 38  
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR\_73:\*\*\*  
2: PIR1:\*\*\*  
3: PIR3:\*\*\*  
4: PIR4:\*\*\*

Prod No. is the number of results predicted by change to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	29	53.7	20	2	tray protein - Esc
2	25	46.3	17	2	photosystem II ext
3	24	44.4	20	2	hypothetical prote
4	23	42.6	6	2	sperm acrosomal pr
5	23	42.6	13	2	hypothetical prote
6	23	42.6	13	2	hypothetical prote
7	23	42.6	13	2	hypothetical prote
8	23	42.6	13	2	hypothetical prote
9	22	40.7	15	2	transcription elonga
10	22	40.7	15	2	hypothetical prote
11	22	40.7	15	2	protein Q66003 -
12	22	40.7	15	2	protein kinase (EC
13	21	38.8	14	2	hypothetical prote
14	21	38.8	14	2	hypothetical prote
15	20	37.0	11	2	epsilon receptor m
16	20	37.0	11	2	T-cell receptor be
17	20	37.0	11	2	ribosomal protein
18	20	37.0	11	2	ribosomal protein
19	20	37.0	11	2	myosin light chain
20	20	37.0	11	2	of 41 - phage T
21	20	37.0	11	2	hypothetical prote
22	19	35.2	13	2	cytochrome oxidase
23	19	35.2	13	2	labelin 1 isoform
24	19	35.2	13	2	neurotransin - bovi
25	19	35.2	13	2	chaperone, TCP1-re
26	19	35.2	13	2	cytochrome oxidase
27	19	35.2	13	2	protein QF200044 -
28	19	35.2	13	2	casein kinase II (
29	19	35.2	13	2	T-cell receptor be

30	19	35.2	18	2	PS0387	platelet derived g
31	19	35.2	18	2	A45139	aspartate oxidase I
32	19	35.2	18	2	S16442	acylating agent
33	19	35.2	20	2	A37111	ribulose biphosph
34	19	35.2	20	2	A56046	urinary tract von
35	18	33.3	10	2	A42089	transcription fact
36	18	33.3	11	2	F04267	ribosomal protein
37	18	33.3	12	2	S01222	transcription elonga
38	18	33.3	15	2	S07987	cytochrome oxidase
39	18	33.3	16	2	F44988	chitinase (EC 3.2.
40	18	33.3	16	2	A59185	multicystatin - 10
41	18	33.3	18	2	A28866	glutathione S-trans
42	18	33.3	18	2	S45373	translation elonga
43	18	33.3	19	2	B16529	lactate dehydrogen
44	18	33.3	20	2	S28405	lamin B receptor -
45	18	33.3	20	2	F00557	acylhydrolase acti

#### ALIGNMENTS

##### RESULT 1

S16478 tray protein - Escherichia coli plasmid incFV (fragment)

C/Species: Escherichia coli

C/Date: 13-Mar-1997 #sequence\_revision 25 Apr-1997 #text\_change 27-Apr-1997

C/Accession: S16478

Fidi laurentis, L., Frost, L.S., Finlay, B.B., Fairclough, W.

Mol Microbiol. 5: 1779-1790, 1991

A/Title: Characterization of the *oriT* region of the *incFV* plasmid pMD208.

A/Reference number: S16478, M01D 1204497, PMID 1341709

A/Accession: S16478

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-20 <LAU>

A/Cross-References: EMBL:X59611

C/Genetics:

A/Genome: plasmid incFV

Query Match 53.7% Score 29; DB 2; Length 20;

Best Local Similarity 62.5%; Prod. No. 52;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKPKNH 10

Db 2 KKPKNH 9

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platelet derived g  
aspartate oxidase I  
acylating agent  
ribulose biphosph  
urinary tract von  
transcription fact  
ribosomal protein  
transcription elonga  
cytochrome oxidase  
chitinase (EC 3.2.  
multicystatin - 10  
glutathione S-trans  
translation elonga  
lactate dehydrogen  
lamin B receptor -  
acylhydrolase acti



QY 3 KKKPK 9  
| | | |  
| | | |  
Db 8 KKKPK 14

## RESULT 9

D28551

Hypothetical protein 4 - Streptococcus mutans (strain GS-5) (fragment)

C:Species: Streptococcus mutans

C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 15-Oct-1999

C:Accession: D28551

R:Shirota, T.; Katsube, H.K.

J. Bacteriol. 170, 419-426, 1992

A:Title: Sequence analysis of the Streptococcus mutans fructosyltransferase gene and the

A:Reference number: A1937, with 441184, F0123325

A:Accession: D28551

A:Molecule type: DNA

A:Reference number: A1937, with 441184, F0123325

A:Accession: D28551

A:Status: preliminary

A:Cross-references: GB:M18954, NID:915375, PIRN:AAA889pe.1, P10:J106027

Query Match

Best Local Similarity 40.7%; Score 22; DB 2; Length 12;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASPPPK 11

| | | | |

| | | | |

Db 2 ANKKRIRLKA 12

## RESULT 10

P10082

Protein Q60000.1: Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 06-Jun-1997

C:Accession: P10082

R:Ragusa, A.; Kato, M.; Kawakami, M.; Oki, Y.

submitted to JIPID, December 1995

A:Reference number: PNU113

A:Accession: P10082

A:Molecule type: protein

A:Residues: 1-15 &lt;STO&gt;

A:Experimental source: leaf

Query Match

Best Local Similarity 40.7%; Score 22; DB 2; Length 15;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASPPPK 11

| | | | |

| | | | |

Db 1 ATIKPKLIXA 11

## RESULT 11

I45957

Protein kinase (EC 2.7.1.37), CAMP-dependent, type I-alpha regulatory chain - bovine (fr

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 18-Jun-1999

C:Accession: I45957

R:Lee, D.C.; Carmichael, D.F.; Krebs, E.G.; McKnight, G.S.

Proc. Natl. Acad. Sci. U.S.A. 90, 3509-3512, 1993

A:Title: Isolation of a cDNA clone for the type I regulatory subunit of bovine CAMP-depe

A:Reference number: I45957; M01D:8322645, PMID:6190178

A:Accession: I45957

A:Status: preliminary; translated from GB/EMBL/DD84

A:Molecule type: mRNA

A:Residues: 1-19 &lt;LEB&gt;

A:Cross-references: DE:K0333, NID:915375, PIRN:AAA889pe.1; F0123325

C:Superfamily: CAMP-dependent protein kinase regulatory chain, CAMP receptor protein cyd

C:Keywords: phosphotransferase

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKPK 10

| | | |

| | | |

Db 2 KAKTKVK 8

## RESULT 12

H83778

Hypothetical protein B1032 (imported) - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 18-Jun-2001

C:Accession: H83778

R:Ragusa, A.; Kato, M.; Kawakami, M.; Oki, Y.

submitted to JIPID, December 1995

A:Reference number: A1937, with 441184, F0123325

A:Accession: H83778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-14 &lt;STO&gt;

A:Cross-references: GB:M18954, NID:915375, PIRN:AAA889pe.1, P10:J106027

A:Experimental source: strain C-125

C:Keywords: lymphocyte

Query Match

Best Local Similarity 38.9%; Score 21; DB 2; Length 14;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKPK 7

| | | |

| | | |

Db 2 KKKPK 6

## RESULT 13

PX0031

mixed lymphocyte reaction inhibitor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 24-Feb-1993

C:Accession: PX0031

R:Shimomura, T.; Ohara, T.; Wada, N.; Omeri, A.; Kamada, N.

J. Biochem. 107, 435-439, 1990

A:Title: Rat liver arginase suppresses mixed lymphocyte reaction.

A:Reference number: PX0031; M01D:90256720, PMID:2140155

A:Accession: PX0031

A:Molecule type: protein

A:Residues: 1-15 &lt;SHI&gt;

A:Experimental source: liver

C:Keywords: lymphocyte

Query Match

Best Local Similarity 80.0%; Score 21; DB 2; Length 15;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SKKPK 6

| | | |

| | | |

Db 8 SKKPK 12

## RESULT 14

A61220

epilium receptor modulating protein (F1-3422) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Mar-1996

C:Accession: A61220

R:Matsumura, S.; Tazaki, D.H.

Cell Immunol. 137, 252-259, 1991

A:Title: The murine epilium receptor modulating protein: a novel serine protease which m

A:Reference number: A61220, M01D:21556570, PMID:1679381

A:Accession: A61220

A:Molecule type: protein

A:Residues: 1-18 &lt;MAT&gt;

1. Name: This serine protease from a T cell hybridoma does not reduce levels of CD23  
 2. Enzyme: hydrolase; serine protease

Query Match 88.9%; Score 21; DB 2; Length 18;  
 Best Local Similarity 45.9%; Pred. No. 1.6e+03;  
 Mismatch 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

27 1 ASKRRRIKA 11  
 1 1 1 1 1  
 1b 4 ASKRRRIKA 14

SEQUENCE 15

1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

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1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

1b 11 T cell receptor beta chain V D J region (clone 10) - rat (fragment)

GenCore version 5.1.4 P5 4578  
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ON FILE: FILEIN SEARCH, USING SW MBLBL

Run: March 20, 2003, 09:40:26, Search time: 11 seconds

(without alignments)  
41,476 Million total updates/sec

Title: US-09-787-443-1

Sequence: 1 ASKRPENIKA 11

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Search: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum March 03

Maximum March 1998

Listing first 45 summaries

Database: SwissProt\_40\*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length (aa)	Hit	Description
1	29	63.7	TRYS_ECOLI	233898 Escherichia
2	24	49.1	PS19_PWBWP	Q67094 Pigeon pea
3	24	44.4	HE_COTJA	P18638 cottonin co
4	21	38.9	PSF_BACCE	P13078 bacillus co
5	20	47.0	844E_P3031	844E_P3031
6	20	37.0	CS15_BACSO	CS15_BACSO
7	20	37.0	NCB_MACE	NCB_MACE
8	19	35.2	MMPX_SOUTU	MMPX_SOUTU
9	19	35.2	AL13_CAWMA	AL13_CAWMA
10	19	35.2	MIFH_TRISP	MIFH_TRISP
11	19	35.2	ACRH_BOVIN	ACRH_BOVIN
12	18	33.3	COXC_PAVIT	COXC_PAVIT
13	18	33.3	PS19_CLOBP	PS19_CLOBP
14	18	33.3	PS19_LOWER	PS19_LOWER
15	18	33.3	PS19_LOWER	PS19_LOWER
16	18	33.3	PS19_LOWER	PS19_LOWER
17	18	33.3	PS19_LOWER	PS19_LOWER
18	18	33.3	PS19_LOWER	PS19_LOWER
19	18	33.3	PS19_LOWER	PS19_LOWER
20	18	33.3	PS19_LOWER	PS19_LOWER
21	18	33.3	PS19_LOWER	PS19_LOWER
22	18	33.3	PS19_LOWER	PS19_LOWER
23	18	33.3	PS19_LOWER	PS19_LOWER
24	18	33.3	PS19_LOWER	PS19_LOWER
25	18	33.3	PS19_LOWER	PS19_LOWER
26	18	33.3	PS19_LOWER	PS19_LOWER
27	18	33.3	PS19_LOWER	PS19_LOWER
28	18	33.3	PS19_LOWER	PS19_LOWER
29	18	33.3	PS19_LOWER	PS19_LOWER
30	18	33.3	PS19_LOWER	PS19_LOWER
31	18	33.3	PS19_LOWER	PS19_LOWER
32	18	33.3	PS19_LOWER	PS19_LOWER
33	18	33.3	PS19_LOWER	PS19_LOWER

34	16	29.6	12	1	SO15_BACSU	pa0441 bacillus su
35	16	29.6	13	1	BLAC-STECR	pa1173 streptococ
36	16	29.6	14	1	PS19_PWBWP	pa1173 streptococ
37	16	29.6	15	1	ACERACTIOA	pa1173 streptococ
38	16	29.6	16	1	ONC1_CONMY	pa1173 streptococ
39	16	29.6	17	1	PS19_PWBWP	pa1173 streptococ
40	16	29.6	18	1	COXC_THOSE	pa1173 streptococ
41	16	29.6	19	1	PSAF_MALZE	pa1173 streptococ
42	16	29.6	20	1	PSAF_MALZE	pa1173 streptococ
43	16	29.6	21	1	PSAF_MALZE	pa1173 streptococ
44	16	29.6	22	1	PSAF_MALZE	pa1173 streptococ
45	16	29.6	23	1	PSAF_MALZE	pa1173 streptococ

#### ALIGNMENTS

RESULT 1	TRYS_ECOLI	STANDARD;	PRT;	20 AA.
ID	TRYS_ECOLI			
AC	ps1788			
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DT	01-FEB-1994 (Prl 31, last sequence update)			
DT	01-FEB-1994 (Prl 31, last annotation update)			
DE	Tryp protein (Fragment).			
OS	TRAY.			
OS	Escherichia coli			
OC	plasmid incv pdd208.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
FN	[1]			
PP	SEQUENCE FROM N A			
FX	MENTINE:204497, PubMed:1943709;			
PA	di laurentio L, Prost L S, Finlay B R, Paranchych W;			
RT	"Characterization of the virulence of the T4V plasmid pdd208."			
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15 100% identical (P. 1000 82) (Fragment).  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 1 ACPPR 2  
 2 ACPPR 2  
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OY 6 KPN1 9  
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 Db 5 KPN1 9

## RESULT 6

CSIS\_BACSU  
 ID CSIS\_BACSU STANDARD; PRT: 11 AA.  
 AC P81055;  
 DT 15-JUL-1998 (Ref. 36, Created)  
 DT 15-JUL-1998 (Ref. 36, Last sequence update)  
 DT 15-JUN-2002 (Ref. 41, Last annotation update)  
 DE Cold shock protein CSIS (11 kDa cold shock protein) (Fragment).  
 OS Bacillus subtilis.  
 NC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus  
 NC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE  
 RC STPAIN-19 / JH42;  
 RA Graumann P I, Schmidt P, Marahiel M A;  
 PL Submitted (OCT-1997) to the SWISS-PROT data bank  
 RN [2]  
 RP CHARACTERIZATION  
 RC STPAIN-169 / JH42;  
 RA MEDLINE=96345629; PubMed=8755892;  
 RA Graumann P, Schroeder V, Schmidt P, Marahiel M A;  
 RT Cold shock stress-induced proteins in Bacillus subtilis";  
 PL Bacteriol 178:4411-4419(1996)  
 RN [3]  
 RP SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- LOCATION: IN RESPONSE TO LOW TEMPERATURE  
 FT NON TER 11  
 SO SEQUENCE 11 AA; 1360 MW; 156F8E64707330 CRC64;

Query Match 37.0%; Score 20; DB 1; Length 11;  
 Best Local Similarity: 100.0%; Pred No 4 Cons; 0  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 7 RNK1 10  
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 Db 2 RNK1 5

## RESULT 7

MDH\_ACIDE  
 ID MDH\_ACIDE STANDARD; PRT: 17 AA.  
 AC P81816;  
 DT 01-FEB-1996 (Ref. 33, Created)  
 DT 01-FEB-1996 (Ref. 33, Last sequence update)  
 DT 15-OCT-2001 (Ref. 40, Last annotation update)  
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).  
 GN MDH.  
 OS Acidovorax delafieldii  
 NC Bacteria; Proteobacteria; beta subdivision; Gammaproteobacteria;  
 NC Acidovorax  
 CC MEDLINE=97334132; PubMed=9190829;  
 RN [1]  
 RP SEQUENCE  
 RC STPAIN-CCUG 12929;  
 RA MEDLINE=97334132; PubMed=9190829;  
 RN [2]  
 RP CHARACTERIZATION  
 RC "Structural studies of malate dehydrogenases (MDHs): MDHs in  
 RT Frevindromonas species are the first reported MDHs in Proteobacteria  
 RT which resemble lactate dehydrogenases in primary structure";  
 PL Bacteriol 179:4066-4070(1997)  
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) -> oxaloacetate + NADH.  
 CC -1- SIMILARITY: BELONGS TO THE LHM FAMILY MDH SUBFAMILY.  
 CC Interpro: Ippro1350; MB  
 CC PROSITE: P00064; MDH; PARTIAL  
 CC OX13503:1350; TrntrnXy13:13 OY:16; MAD  
 FT NON TER 17  
 SO SEQUENCE 17 AA; 1662 MW; 110E811AC16992E CRC64;

Query Match 37.0%; Score 20; DB 1; Length 17;  
 Best Local Similarity: 80.0%; Pred No 7c+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 KKPPE 7  
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 Db 2 KKPPE 6

## RESULT 8

MMFX\_SOLTU  
 ID MMFX\_SOLTU STANDARD; PRT: 16 AA.  
 AC P80501;  
 DT 01-FEB-1996 (Ref. 33, Created)  
 DT 01-FEB-1996 (Ref. 33, Last sequence update)  
 DT 01-NOV-1997 (Ref. 35, Last annotation update)  
 DE Unidentified mitochondrial matrix protein (Fragment).  
 OS Solanum tuberosum (Potato).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 CC Asteridae; Euasteride I; Solanales; Solanaceae; Solanum.  
 NC NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Tuber;  
 RX MEDLINE=97077345; PubMed=8919912;  
 PA Tansch L, Kruf V, Schmitz H V, Braun H P;  
 RT "New insights into the composition, molecular mass and stoichiometry  
 PT of the protein complexes of plant mitochondria";  
 PL Plant J 9:357-368(1996)  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KM Mitochondrion.  
 FT NON TER 16  
 SO SEQUENCE 16 AA; 1768 MW; C58D4DB48A19B8D CRC64;

Query Match 35.0%; Score 19; DB 1; Length 16;  
 Best Local Similarity: 40.0%; Pred No 1e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ASKPKRNIX 10  
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 Db 1 ASNPKEIVE 10

## RESULT 9

AL13\_CARMA  
 ID AL13\_CARMA STANDARD; PRT: 18 AA.  
 AC P81816;  
 DT 30-MAY-2000 (Ref. 39, Created)  
 DT 30-MAY-2000 (Ref. 39, Last sequence update)  
 DT 30-MAY-2000 (Ref. 39, Last annotation update)  
 DE Carcinus statin 13.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
 CC Malacostraca; Eumalacostraca; Decapoda; Decapoda; Decapoda;  
 CC Eumalacostraca; Eumalacostraca; Eumalacostraca; Eumalacostraca;  
 CC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121123; PubMed=9461295;  
 RX Dive H, Johnson A H, Maestre J L, Scott A G, Taro P P,  
 RA Thorpe A;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas";  
 PL Eur J Biochem 250:727-734(1997)  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Neuropeptide family.  
 FT MOD RES 18  
 SO SEQUENCE 18 AA; 2235 MW; 35A110C8160A27 CRC64;

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37 MEDLEY, J. G. 1969, *Polym.* 10:4786.  
 38 BARNER, J. C., BUCKLE, J. M., BUCKLE, Q. D., DODD, F., GLENN, P. F.,  
 39 JAMES, R. E., JORDAN, L. W., SCHICK, M. E., SHAN, Y., MOYER, D. L.,  
 40 "wound purification and characterization of a degradative methyl ester  
 41 of a protective (methylol) reaction inhibitory factor" from *Trichinella*  
 42 *spiralis*, *Trichinella* spp. and *Trichinella* sp.  
 43 *Journal of Parasitology*, 1984.  
 44 1. ENZYME CATALYTIC ACTIVITY OF THE METHYL ESTER OF L-TRYPTOPHAN  
 45 1. IMPORTANCE INHIBITED BY FREE FATTY ACIDS AND BARIUM.  
 46 2. SIMILARITY BETWEEN THE MIF FAMILY.  
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12  -1- PROTEIN: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
13  -1- ESTERAL BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
14  -1- AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO TERMINUS.
15  -1- PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
16  -1- CATALYTIC ACTIVITY: Aminoacyl-peptidase. H2O + acylamino acid
17  -1- + peptide.
18  -1- SOURCE: HOMOIOPEP.
19  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 50.
20  -1- PIR: S36842; S36842.
21  -1- InterPro: IPR002471; Pro1 embedded seq.
22  -1- Pfam: PF00703; PRO_PEPFAM_SEQ, PARTIAL.
23  -1- K1 Hydrolyase.
24  -1- NON_TER 1
25  -1- FT NON_TER 20
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OY      4 KRENIE 10
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Db

RESULT 12
COXQ_PABIT
COXQ_PABIT COXQ_PABIT STANDARD; FET, 10 MA.
AC P80336;
PT 01-OCT-1994 (Ref. 30, Created)
PI 01-OCT-1994 (Ref. 30, Last sequence update)
PT 16-JUN-2002 (Ref. 41, Last annotation update)
FE 37-01176 - 41base P 3)Ref:100 V101.1167;Heart (EC 1.9.3.11
DE (Fragment).
COX8H.
GN COX8H.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;
OC Mammalia; Eulagomorpha; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxId:9586;

```

RP	SEQUENCE	
RC	TISSUE=Heart, and Liver;	
PA	Fr-104 P. Kottbach B.;	
PL	Submitted (May-1984) to the Swiss Prot. data bank.	
CC	1. FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE CHAINS OF MITOCHONDRIAL OXIDATIVE PHOSPHORYLATION. THE TERMINAL CYSTINE IN MITOCHONDRIAL ELECTRON TRANSPORT.	
CC	1. CATALYTIC ACTIVITY: 4 ferredoxin:cytochrome c + 2 H <sub>2</sub> O.	
CC	1. SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE WITH FAMILY.	
KM	Oxidation state: Mitochondrion.	
ET	NOV TER	10
SL	SEQUENCE	10 AA; 1007 MW; 27675440076136 TFC64;

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Query Match 33.8% Score 187 DB 1; length 10;
Pct Ident Similarity 67.9% Pct Ident 100.00%
Matches 4 Conservative 0 Mismatches 2 Indels 0 Gaps 0
OY      2 SKPPER 7
        |||||
Pr       2 GKPPAR 7

RESULT 13
RS19 ClOPP STANDARD; PRT: 14 AA.
AC Q46Z28;
DT 30-MAY-2006 (Rel. 39, Created)
DT 30-MAY-2006 (Rel. 39, last sequence update)
DT 30-MAY-2006 (Rel. 39, last annotation update)
DE 30c ribosomal protein s19 (Fragment).
CE RPS8 OR RPS19
CN Clover proliferation phytoplasmata.
OS

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CC Bacteria; Firmicutes; Mollicutes; Achaeplastatales;  
 CC Achaeplastatales; Phytolasma.  
 CC NCBI\_TaxID=35776;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=9435090; PubMed=8071198;  
 CC Gundersen D.E., Lee I.M., Rehner S.A., Davis P.F., Kingsbury D.T.;  
 CC Phylogeny of mycoplasma-like organisms (phytoplasmatales), a basis for  
 CC their classification.  
 CC RT Bacteriol. 176:5244-5254(1994).  
 CC -1- FUNCTION: PROTEIN S13 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -1- SIMILARITY: RELATES TO THE S13 FAMILY OF RIBOSOMAL PROTEINS.  
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 CC EMBL: L27011; AAA9394.1;  
 CC InterPro: IPR002222; Pfam: P00001\_S13;  
 CC EC00787; Pfam: P00001\_S13; PARTIAL.  
 CC P00001: Protein, rRNA-binding.  
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 CC Best Local Similarity 44.4%; Pred. No. 1.4e+03;  
 CC Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
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 CC QY 2 SKPPENIK 10  
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 CC Db 5 AKGDKKXK 13  
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 CC RS19\_LUMEP STANDARD; PRT; 14 AA.  
 CC AC 048878;  
 CC DT 30-MAY-2000 (rel. 39, Created)  
 CC DT 30-MAY-2000 (rel. 39, Last sequence update)  
 CC DT 30-MAY-2000 (rel. 39, Last annotation update)  
 CC DT 108 Ribosomal protein S13 (fragment).  
 CC PPS8 OR PPS19.  
 CC Locofah w/ches; -broom phytoplasmatales.  
 CC Bacteria; Firmicutes; Mollicutes; Achaeplastatales;  
 CC Achaeplastatales; Phytolasma.  
 CC NCBI\_TaxID=35773;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=9435090; PubMed=8071198;  
 CC Gundersen D.E., Lee I.M., Rehner S.A., Davis P.F., Kingsbury D.T.;  
 CC Phylogeny of mycoplasma-like organisms (phytoplasmatales), a basis for  
 CC their classification.  
 CC RT Bacteriol. 176:5244-5254(1994).  
 CC -1- FUNCTION: PROTEIN S13 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -1- SIMILARITY: RELATES TO THE S13 FAMILY OF RIBOSOMAL PROTEINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L27027; AAA9394.1;  
 CC InterPro: IPR002222; Pfam: P00001\_S13;  
 CC P00001: Protein, rRNA-binding.  
 CC FT NON TER 1 1  
 CC SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

KW Ribosomal protein; rRNA-binding.  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;  
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 CC Best Local Similarity 44.4%; Pred. No. 1.4e+03;  
 CC Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
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 CC QY 2 SKPPENIK 10  
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 CC Db 5 AKGDKKXK 13  
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 CC RESULT 15  
 CC COX1\_THUOB STANDARD; PRT; 15 AA.  
 CC ID COX1\_THUOB  
 CC AC P80978;  
 CC DT 01-NOV-1997 (rel. 35, Created)  
 CC DT 01-NOV-1997 (rel. 35, Last sequence update)  
 CC DT 01-NOV-1997 (rel. 35, Last annotation update)  
 CC DE Cytochrome c oxidase polypeptide vic-2 (EC 1.9.3.1) (fragments).  
 CC OS Thunnus obesus (Bigeye tuna).  
 CC EC EnzymeCat: Oxidat; Oxidat; Oxidat; Oxidat; Oxidat; Oxidat;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;  
 CC Scombridae; Thunnus.  
 CC NCBI\_TaxID=8241;  
 CC [1]  
 CC SEQUENCE  
 CC RP TISSUE=Heart;  
 CC RC MEDLINE=97454291; PubMed=9310366;  
 CC PA Arnold S., Lee I., Kim M., Song F., Linde P., Lottspeich F.,  
 CC RA Kadenbach B.;  
 CC RT "The subunit structure of cytochrome c oxidase from tuna heart and  
 CC liver."  
 CC EMBL: B10000.248:99-103(1997).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferri-cytochrome c + 4 e- + 2 H2O  
 CC CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC KM oxidoreductase; Inner membrane; Mitochondrion.  
 CC FT NON TER 1 1  
 CC FT NON CONS 8 9  
 CC FT NON TER 15 15  
 CC SEQUENCE 15 AA; 1696 MW; 4C4C966C73A40294 CRC64;  
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 CC Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 2 SKPP 5  
 CC :|||  
 CC Db 7 AKKP 10  
 CC  
 CC Search completed: March 20, 2003, 09:41:33  
 CC Job time : 14 secs

The first of these is the fact that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The second is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The third is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The fourth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The fifth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The sixth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The seventh is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The eighth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The ninth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The tenth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

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Run on: March 20, 2003, 09:40:31, Search time 29 seconds

(without alignments)  
78,156 Million cell sequences

File: US-09-787-443-1

Sequence: 1 ASKPPRNIVA 11

Scoring table: BLOSUM62

Gap: 10, Gapext: 0.5

Database: GenCore seqs, 20030315

Total number of hits satisfying the criteria: 6175

Minimum hit seq length: 10  
Maximum DB seq length: 20

Post processing: Minimum March 08  
Maximum March 1008

Listing first 45 summaries

Database:

SPREMBL\_21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_virus:  
12: sp\_vertebrate:  
13: sp\_unclassified:  
14: sp\_virus:  
15: sp\_bacteriophage:  
16: sp\_bacteriophage:  
17: sp\_archaea:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the score distribution.

# SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	29	51.9	17	5	Q9TWR3
2	26	48.1	15	2	Q9AF0
3	25	45.3	15	13	Q9AF0
4	24	44.4	17	4	Q9UC6
5	24	44.4	17	6	Q9TWR3
6	24	44.4	15	4	Q9TWR3
7	23	42.6	9	9	Q9TWR3
8	23	42.6	15	3	Q9TWR3
9	23	42.6	15	4	Q9TWR3
10	23	42.6	15	4	Q9TWR3
11	22	40.7	15	11	Q9TWR3
12	22	40.7	15	11	Q9TWR3
13	22	40.7	15	11	Q9TWR3
14	22	40.7	15	11	Q9TWR3
15	22	40.7	15	11	Q9TWR3
16	22	40.7	15	11	Q9TWR3

17	22	40.7	15	12	Q9TWR3
18	22	40.7	15	12	Q9TWR3
19	22	40.7	15	12	Q9TWR3
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45	22	40.7	15	12	Q9TWR3

## ALIGNMENTS

### RESULT 1

ID Q9TWR3 PRELIMINARY: PRT: 17 AA.  
AC Q9TWR3  
DT 01-MAY-2000 (TREMURel\_13, Created)  
DT 01-MAY-2000 (TREMURel\_13, Last sequence update)  
DT 01-MAY-2000 (TREMURel\_14, Last annotation update)  
DE Histone H1 (Fragment).  
OS Trypanosoma cruzi.  
CC Eukaryota, Eukaryota, Eukaryota, Trypanosoma, Trypanosoma.  
CN NCBI\_Taxid=5693;  
RN [1]  
RP  
BX MEDLINE=94041510; PubMed=8227175;  
PA Toro G C, Galanti N, Hellman U, Wernstedt C,  
PT "Unambiguous identification of histone H1 in Trypanosoma cruzi."  
PI J Cell Biochem 53:413-419(1993).  
SQ SEQUENCE 17 AA, 1620 MW, ALKSRSSDSEKSTSS QKQ4;  
Q9TWR3

Query March 51.98; Score 28; DB 5; Length 17;

Best Local Similarity 50.00; Pred No 1; Length 17;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKPPRNIVA 10

Lb 1 ASKPPRNIVA 11

Q9TWR3 PRELIMINARY: PRT: 17 AA.

DT 01-MAY-2000 (TREMURel\_13, Created)

DT 01-MAY-2000 (TREMURel\_13, Last sequence update)

DT 01-MAY-2000 (TREMURel\_13, Last annotation update)

DE Desulfovibrio vulgaris, Delta subunit (Fragment).

[illegible]

```

Cy      3 REPENIN 10
      :|:|:|:|
Db      4 EXPEKVV 11

Query Match      44.4% Score 24; DB 4; Length 17;
Best Local Similarity 37.5% Pred No. 8.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0

RESULT 5
Q9TR21
ID Q9TR21; PRELIMINARY; PRT; 17 AA.
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14; Last annotation update)
DE Pleiotrophin (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivordia; Suidae; Sus.
CY NCBI_TaxId=96063;
RN [1]
RP SEQUENCE.
RX MEDLINE=26165077, PubMed=8568456;
FA Birgestock D.P., Kim G.Y., Steffen C.L.;
PT "P3 late-line luminal fluid contains the developmentally regulated
PT neurotrophic factor, pleiotrophin."
PI 1 Endocrinol 149:101-110(1996).
SQ SEQUENCE 17 AA; 1978 MW; 524165BFF417AD6 CRC64;

Query Match      44.4% Score 24; DB 6; Length 17;
Best Local Similarity 37.5% Pred No. 8.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0

Cy      3 REPENIN 10
      :|:|:|:|
Db      4 EXPEKVV 11

Query Match      44.4% Score 24; DB 4; Length 19;
Best Local Similarity 37.5% Pred No. 9.6e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0

RESULT 6
Q9UCN8
ID Q9UCN8; PRELIMINARY; PRT; 19 AA.
AC Q9UCN8;
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14; Last annotation update)
DE Osteoblast-specific factor 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Hominidae; Homo.
CY NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=36887099, PubMed=109459;
FA Takamatsu H., Itoh M., Kimura M., Otsuhashi T.;
PT "Expression and purification of biologically active human ODF-1 in
PT Escherichia coli".
SC Escherichia coli;
CY NCBI_TaxId=562;
SQ SEQUENCE 19 AA; 2040 MW; 1987A4D70585F741 CRC64;

Query Match      44.4% Score 24; DB 4; Length 19;
Best Local Similarity 37.5% Pred No. 9.6e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0

Cy      3 REPENIN 10
      :|:|:|:|
Db      4 EXPEKVV 11

```



[illegible][illegible]

Thu Mar 20 13:48:45 2003

us-09-787-443-1.rpt

Page 5

db 2 KPR 5

Search completed: March 20, 2003, 09:48:53  
Job time : 30 secs





GenCore version 5.1.4 ps 4578  
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OM protein - protein search, using sw model

Run on: March 20, 2003, 09:41:01, Search time 15 seconds

(without alignments)  
21 577 Million cell updates/sec

**Title:** US-09-787-443-1

**Perfect score:** 54

**Sequence:** 1 ASKRPENIKK 11

Scoring table: BLOSUM62

Gapop: 10 0, Gapext: 0 5

Searched: 262574 seqs, 29422922 residues 132970

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

**Database:**

1: /gen2\_6/prodata/2/1aa/5A/COMB.pep.\*  
2: /gen2\_6/prodata/2/1aa/5B/COMB.pep.\*  
3: /gen2\_6/prodata/2/1aa/5A/COMB.pep.\*  
4: /gen2\_6/prodata/2/1aa/5B/COMB.pep.\*  
5: /gen2\_6/prodata/2/1aa/COMB.pep.\*  
6: /gen2\_6/prodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query Match Length	DB ID	Description
1	33	61.1	11 1	US-08-116-733-31
2	29	53.7	11 1	US-08-116-733-1
3	29	53.7	11 1	US-08-116-733-32
4	29	53.7	11 1	US-08-116-733-39
5	29	53.7	11 1	US-08-116-733-48
6	29	53.7	11 1	US-08-116-733-41
7	29	53.7	13 1	US-08-116-733-30
8	28	51.9	9 1	US-08-116-733-45
9	28	51.9	11 1	US-08-116-733-36
10	28	51.9	11 2	US-08-856-661 9
11	28	51.9	11 1	US-08-193-521 16
12	28	51.9	11 1	US-08-434-122 104
13	28	51.9	18 4	US-08-465-325-102
14	28	51.9	18 4	US-09-115-737-103
15	28	51.9	19 1	US-09-556-823-5
16	27	50.0	15 3	US-08-041-899-17
17	27	50.0	15 3	US-08-837-058-17
18	27	50.0	18 2	US-08-841-483-15
19	27	50.0	18 2	US-08-841-483-16
20	27	50.0	19 4	US-09-392-911-15
21	27	50.0	19 4	US-09-392-911-16
22	27	50.0	20 1	US-08-498-210A-29
23	27	50.0	20 1	US-08-498-210A-29
24	27	50.0	20 2	US-09-329-206-29
25	27	50.0	20 2	US-08-498-209B-28
26	27	50.0	20 2	US-08-498-211-28
27	26	48.1	9 2	US-08-934-222-85
28	26	48.1	9 2	US-08-933-402-85

29	26	48.1	9 2	US-08-297-621 95	Sequence 87, Appl
30	26	48.1	9 2	US-08-532-818 95	Sequence 88, Appl
31	26	48.1	9 3	US-08-231-797-85	Sequence 89, Appl
32	26	48.1	9 3	US-08-934-224 85	Sequence 89, Appl
33	26	48.1	9 3	US-08-933-843-85	Sequence 89, Appl
34	26	48.1	9 4	US-08-934-223-85	Sequence 89, Appl
35	26	48.1	9 4	US-08-413-492-85	Sequence 89, Appl
36	26	48.1	10 1	US-08-401-512-57	Sequence 57, Appl
37	26	48.1	15 3	US-08-466-860-13	Sequence 11, Appl
38	26	48.1	15 3	US-08-472-240A-13	Sequence 13, Appl
39	26	48.1	15 4	US-08-276-776-13	Sequence 13, Appl
40	26	48.1	17 4	US-08-471-209-13	Sequence 13, Appl
41	26	48.1	18 2	US-08-894-329-4	Sequence 42, Appl
42	26	48.1	18 2	US-08-306-044-4	Sequence 4, Appl
43	25	46.3	15 3	US-08-641-889-18	Sequence 19, Appl
44	25	46.3	15 3	US-08-837-058-18	Sequence 18, Appl
45	25	46.3	20 4	US-08-242-221A-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-116-733-31  
Sequence 31, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALMER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESS: NIXON & VANCEPHE P.C.

STREET: 1100 NORTH GREEK ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

PREFERENCE/DOCKET NUMBER: 1573-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 280797 NIXN UR

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-31

Query Match

Best Local Similarity 61.1%; Score 33; DB 1; Length 11;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASKRPEN 8

DE 1 ATKRPEN 8

REPORT 1  
US-08-116-733-39  
Application US/08/08116733  
Patent No. 5516632  
INVENTOR: PAIKER, THOMAS J.  
APPLICANT: HAYNES, BARTON F.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES  
NUMBER OF SEQUENCES: 46  
PRIORITY NUMBER: 46  
ADDRESS: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
MOLECULE TYPE: PEPTIDE  
METHOD TYPE: FLOPPY disk  
METHOD: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA  
APPLICATION NUMBER: US/08/08116733  
FILING DATE: 07 SEP 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 22,955  
REFERENCE/DOCKET NUMBER: 1579-33  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4000  
TELEX: 200797 NIXN DR  
INFORMATION FOR SEQUENCE: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-733-39  
Query Match 53.7% Score 29; DB 1; Length 11;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 2 SKIPPEN 8  
DB 2 ARKPNEN 8  
RESULT 4  
US-08-116-733-39  
Seq. No. 39, Appl. No. US/08/08116733  
Patent No. 5516632  
GENERAL INFORMATION:  
APPLICANT: PAIKER, Thomas J.  
APPLICANT: HAYNES, Barton F.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/08116733  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 22,955  
REFERENCE/DOCKET NUMBER: 1579-33  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4000  
TELEX: 200797 NIXN DR  
INFORMATION FOR SEQUENCE: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-733-39  
Query Match 53.7% Score 29; DB 1; Length 11;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 2 SKIPPEN 8

REPORT 1  
US-08-116-733-39  
Application US/08/08116733  
Patent No. 5516632  
INVENTOR: PAIKER, Thomas J.  
APPLICANT: HAYNES, BARTON F.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES  
NUMBER OF SEQUENCES: 46  
PRIORITY NUMBER: 46  
ADDRESS: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
MOLECULE TYPE: PEPTIDE  
METHOD TYPE: FLOPPY disk  
METHOD: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA  
APPLICATION NUMBER: US/08/08116733  
FILING DATE: 07 SEP 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 22,955  
REFERENCE/DOCKET NUMBER: 1579-33  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4000  
TELEX: 200797 NIXN DR  
INFORMATION FOR SEQUENCE: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-733-39  
Query Match 53.7% Score 29; DB 1; Length 11;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 2 SKIPPEN 8

Db :||| ||  
2 TKKPNRN 8

## RESULT 5

US-08-116-733-40

Sequence 40, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-40

Query Match 53.7%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SKKPNRN 8

Db 2 TKKPNRN 8

## RESULT 6

US-08-116-733-41

Sequence 41, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

US-08-116-733-41

Query Match 53.7%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SKKPNRN 8

Db 2 TKKPNRN 8

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-41

Query Match 53.7%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SKKPNRN 8

Db 2 TKKPNRN 8

## RESULT 7

US-08-116-733-30

Sequence 30, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/116,733

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-33

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-116-733-30

Query Match 53.7%; Score 29; DB 1; Length 13;



INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-856-663-8

Query Match 51.9% Score 28; DB 2; Length 11,  
Best Local Similarity 62.5% Pred. No. 41;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKPNIK 9  
||||:|  
Db 1 KKKPNIK 8

RESULT 11  
US-08-193-521-10  
Sequence 103, Application US/084334120  
Patent No. 5470950  
GENERAL INFORMATION:  
APPLICANT: Maloy, W. Lee  
APPLICANT: Karl, U. Prasad  
APPLICANT: Williams, Jon I.  
TITLE OF INVENTION: Biologically Active Peptide  
TITLE OF INVENTION: Compositions and Uses Therefor  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4 V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193,521  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/870,960  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 421250-161  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: May be a C-terminal amide,  
OTHER INFORMATION: and/or may be acetylated at  
OTHER INFORMATION: N-terminus.  
US-08-193-521-10

Query Match 51.9% Score 28; DB 1; Length 18;  
Best Local Similarity 62.5% Pred. No. 66;  
GENERAL INFORMATION:

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 3 KKKPNIK 10  
||||:|  
Db 9 KKKPNIK 16

RESULT 12  
US-08-434-120-104  
Sequence 104, Application US/08434120  
Patent No. 5635479  
GENERAL INFORMATION:  
APPLICANT: Baker, Margaret A.  
APPLICANT: Jacob, Leonard S.  
APPLICANT: Maloy, W. Lee  
TITLE OF INVENTION: Treatment of Gynecological  
TITLE OF INVENTION: Malignancies with  
TITLE OF INVENTION: Biologically Active Peptides  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DM4 V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,120  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,950  
FILING DATE:  
APPLICATION NUMBER: US/08/226,108  
FILING DATE:  
APPLICATION NUMBER: US/07/937,462  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 421250-194  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-434-120-104

Query Match 51.9% Score 28; DB 1; Length 18;  
Best Local Similarity 62.5% Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KKKPNIK 10  
||||:|  
Db 9 KKKPNIK 16

RESULT 13  
US-08-465-325-103  
Sequence 103, Application US/08465325  
Patent No. 5686563  
GENERAL INFORMATION:



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 323-5070  
 TELEFAX: (415) 854-0875  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-556-823-5

Query Match 51.9% Score 26; DB 1; Length 19;  
 Best Local Similarity 71.4%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 4 KPPNIX 10  
 ||| : :  
 Db 1 KPKTNMK 7

Search completed: March 20, 2003, 03:43:41  
 Job time : 17 secs





GenCore version 5.1.4-p5\_4578  
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OW protein - protein search, using sw model

Run on: March 20, 2003, 09:41:41 ; Search time 13 seconds  
(without alignments)

45,237 Million cell updates/sec

US-09-787-443-1  
Perfect score: 54  
Sequence: 1 ASKRPXNPKA 11

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 22153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 45299

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

# Database:

## Published Applications: A1\*

1: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/prodata/2/pubpaa/PC1\_NEW\_PUB pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
6: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
7: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
8: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
9: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
10: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
11: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
12: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
13: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB pep.\*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	61.1	13	10	US-09-730-772-10
2	33	61.1	13	10	US-09-735-849-10
3	28	51.0	9	9	US-10-094-699-44
4	26	48.1	15	9	US-10-092-750-39
5	26	48.1	17	9	US-09-929-724-42
6	25	46.3	20	10	US-09-844-813-1
7	25	46.3	20	10	US-09-844-813-1
8	24	44.4	9	9	US-09-566-193A-15
9	24	44.4	10	10	US-10-108-798-12
10	24	44.4	10	10	US-10-108-798-12
11	24	44.4	10	10	US-10-108-798-12
12	24	44.4	10	10	US-10-108-798-12
13	24	44.4	10	10	US-10-108-798-12
14	24	44.4	10	10	US-10-108-798-12
15	24	44.4	10	10	US-10-108-798-12
16	24	44.4	10	10	US-10-108-798-12
17	24	44.4	10	10	US-10-108-798-12
18	24	44.4	10	10	US-10-108-798-12
19	24	44.4	10	10	US-10-108-798-12

20	24	44.4	20	10	US-09-841-132-230	Sequence 210, App
21	24	44.4	20	10	US-09-841-132-231	Sequence 211, App
22	23	42.6	9	10	US-09-796-234-54	Sequence 24, App1
23	23	42.6	9	10	US-09-872-932-34	Sequence 34, App1
24	23	42.6	15	10	US-09-884-267A-7	Sequence 2, App1
25	23	42.6	16	9	US-09-424-552P-27	Sequence 277, App
26	23	42.6	17	10	US-09-864-761-41554	Sequence 41554, A
27	23	42.6	18	9	US-09-809-341-630	Sequence 630, App
28	23	42.6	18	12	US-10-113-573-2	Sequence 2, App1
29	23	42.6	20	9	US-09-736-457-1834	Sequence 1834, Ap
30	23	42.6	20	9	US-09-903-941-1834	Sequence 1834, Ap
31	23	42.6	20	9	US-09-849-626-1834	Sequence 1834, Ap
32	23	42.6	20	10	US-09-841-132-232	Sequence 232, App
33	23	42.6	20	10	US-09-839-184-10	Sequence 10, App1
34	23	40.7	7	9	US-09-912-165A-50	Sequence 50, App1
35	23	40.7	7	9	US-09-178-296-13	Sequence 13, App1
36	22	40.7	7	9	US-09-861-257-13	Sequence 13, App1
37	22	40.7	7	10	US-09-883-647A-12	Sequence 12, App1
38	22	40.7	9	10	US-09-796-294-35	Sequence 35, App1
39	22	40.7	10	9	US-09-134-793-3	Sequence 3, App1
40	22	40.7	11	9	US-09-949-724-76	Sequence 76, App1
41	22	40.7	11	9	US-10-108-795-28	Sequence 28, App1
42	22	40.7	11	9	US-10-044-995-3	Sequence 3, App1
43	22	40.7	11	10	US-09-839-666-12	Sequence 12, App1
44	22	40.7	11	10	US-09-873-676-16	Sequence 16, App1
45	22	40.7	11	10	US-09-941-611-3	Sequence 3, App1

## ALIGNMENTS

RESULT 1  
US-09-730-772-10  
Sequence 10, Application US-09-730-772  
Patent No. US2001001131A1  
GENERAL INFORMATION:  
APPLICANT: Luyten, Frank P.  
APPLICANT: Moos, Jr., Malcolm  
APPLICANT: Chang, Steven Chao-Huan  
TITLE OF INVENTION: CAPITASE-DERIVED M.EPHROGENETIC  
NUMBER OF SEQUENCES: 24  
REFERENCE ADDRESS:  
ADDRESSEE: Knudsen, Matens, Olson & Bear  
STREET: 620 Newport Center Drive, 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-09-730-772  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/836,081  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bartfeld, Neil S  
REGISTRATION NUMBER: 39,901  
REFERENCE/INVENT NUMBER: N18093-001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid



PRIP FILING DATE: 1997-09-19  
PRIP FILING TIME: 11:00:00  
PRIP APPLICATION NUMBER: 00000000  
PRIP FILING DATE: 1997-09-19

AFRILICANI, NIKOLAY, I. I.  
TITLE OF INVENTION: Kinase Assays Using Polycations  
FILE REFERENCE: 100/07930  
CURRENT APPLICATION NUMBER: US/16/057,912



US-10-042-202-47

Query Match 44.4% Score 24; DB 12; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.8e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKKPKNI 9

DB 4 KKKPKNI 10

RESULT 12

US-09-821-861-11

Sequence 11, Application US/09821861

Publication No. US2003092171A1

GENERAL INFORMATION:

APPLICANT: Schoof, Thomas C.

APPLICANT: Cao, Ximeng

TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT

FILE REFERENCE: 694 47, 132435, 00367

CURRENT APPLICATION NUMBER: US/09/821,861

PRIORITY FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 14

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-09-821-861-11

Query Match 44.4% Score 24; DB 9; Length 14;

Best Local Similarity 55.4%; Pred. No. 2.5e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 3 KKKPKNI 11

DB 4 KKKPKNI 12

RESULT 13

US-10-041-030-17

Sequence 17, Application US/10041030

Patent No. US2003150334A1

GENERAL INFORMATION:

APPLICANT: Powers, Scott

APPLICANT: Mu, David

APPLICANT: Xiang, Phil

APPLICANT: Peng, Yue

APPLICANT: Tuladik Inc.

TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian

FILE REFERENCE: 018761-006810US

CURRENT APPLICATION NUMBER: US/10/041,030

PRIORITY FILING DATE: 2001-11-28

PRIOR APPLICATION NUMBER: US 60/259,503

PRIORITY FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: amino acid

OTHER INFORMATION: sequence identity in comparison of pellino 1 and

US-10-041-030-17

Query Match 44.4% Score 24; DB 12; Length 14;

Best Local Similarity 57.1%; Pred. No. 2.5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKKPKNI 8

DB 1 KKKPKNI 6

RESULT 14

US-09-736-959A-28

Sequence 28, Application US/09736959A

Patent No. US20020076415A1

GENERAL INFORMATION:

APPLICANT: University of Southern California

APPLICANT: Xu, Jing-Hsiung

TITLE OF INVENTION: HEPATITIS C VIRUS GENE PRODUCTS

FILE REFERENCE: 13761-742

CURRENT APPLICATION NUMBER: US/09/736,959A

PRIORITY FILING DATE: 2000-12-14

PRIOR APPLICATION NUMBER: US 60/170,835

PRIORITY FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 16

TYPE: PRT

ORGANISM: Hepatitis C Virus (HCV-1 subtype)

US-09-736-959A-28

Query Match 44.4% Score 24; DB 10; Length 16;

Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKKPKNI 8

DB 9 KKKPKNI 14

RESULT 15

US-09-742-096-16

Sequence 16, Application US/09742096

Patent No. US20020155441A1

GENERAL INFORMATION:

APPLICANT: DROTHER, PIERRE

APPLICANT: DAUBERSTES, PIERRE

TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 200773USODIV

CURRENT APPLICATION NUMBER: US/09/742,096

PRIORITY FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 08/973,642

PRIORITY FILING DATE: 1998-02-06

PRIOR APPLICATION NUMBER: PCT/FR02/00394

PRIORITY FILING DATE: 1996-06-12

PRIOR APPLICATION NUMBER: FR 95/07007

PRIORITY FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 16

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-09-742-096-16

Query Match 44.4% Score 24; DB 9; Length 20;

Best Local Similarity 57.1%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 KKKPKNI 9

DB 6 KKKPKNI 12

Thu Mar 20 13:48:44 2003

us-09-787-443-1.rapb

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Search completed: March 20, 2003, 09:44:03  
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